

RAW SEQUENCE LISTING

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Application Serial Number: 10/80/292
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DATE: 11/29/2004

PATENT APPLICATION: US/10/801,292

TIME: 11:11:32

Input Set : A:\5422-2.app

Output Set: N:\CRF4\11292004\J801292.raw

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3 <110> APPLICANT: LEE, YI-CHAO
4     YUEN, PUI-YEE
5     HUANG, YI-HUEI
6     WU, HUI-CHUAN
8 <120> TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
9     THERAPY OF CANCER
11 <130> FILE REFERENCE: 5422-2
13 <140> CURRENT APPLICATION NUMBER: 10/801,292
14 <141> CURRENT FILING DATE: 2004-03-15
16 <160> NUMBER OF SEQ ID NOS: 21
18 <170> SOFTWARE: PatentIn Ver. 3.2
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21 <211> LENGTH: 2096
22 <212> TYPE: DNA
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28 cocttagtcg cgccccggcc ctcccgtgc ccggagtccg gcggccacga ggcccagccg 180
29 cgtectcccg cgcttgctcg cccggcgggc gcagccatgt cccggggggc cgaggagggtg 240
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32 aaagcctact acgatggagt ggccaagatc ggtgagattg ccaactgggtc ccccggtgtca 420
33 actgaactgg gacatgtcct catagagatt tcaagtaccc acaagaaact caacgagagt 480
34 cttgatgaaa attttaaaaa attccacaaa gagattatcc atgagctgga gaagaagata 540
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37 ggaagccgaa acgcactcaa atatgaacac aaagaaattg agtatgtgga gaccgttact 720
38 tctcgtcaga gtgaaatcca gaaattcatt gcagatggtt gcaaagaggc tctgcttgaa 780
39 gagaagaggc gcttctgctt tctggttgat aagcactgtg gctttgcaaa ccacatacat 840
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43 gtgggttagga aagattacga caccctttct aaatgctcac caaagatgcc ccccgctcct 1080
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45 ccgaattcac aaagggtaaa taattcaaca ggtacttccg aagatccag tttacagcga 1200
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48 ctgctcatcc ccgaggagaa ggatggctgg ctctatggag aacacgacgt gtccaaggcg 1380
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53 cccgagaccg cggctcctaa cgatgccaac gggactgcaa agccgccttt tctcagcgga 1680
54 gaaaaccctt ttgccactgt gaaactccgc ccgactgtga cgaatgatcg ctccggcacc 1740
55 atcattcgat gagaggacag ccaaggactc tcccgggcct ctccggttct cccttgcgga 1800
56 atgatgggcg catcctgtct gccacgtgct gacggtcggg aagcttcagt ggagaggcct 1860
57 aactctaata tgccctgctt aagcaaatca tgcttctctg ttacacgtag ttggggttgac 1920
58 aagtttctgc ctttaagata aatgagtaat agtctaataa ccagctcagc catttaaaat 1980
59 attttcttcc tattctgttc aagaaacagt aaacttggtt tcaatcttta aaaaaaaaaa 2040
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73 20 25 30
75 Leu Gly Lys Asn Tyr Glu Lys Ala Val Asn Ala Met Ile Leu Ala Gly
76 35 40 45
78 Lys Ala Tyr Tyr Asp Gly Val Ala Lys Ile Gly Glu Ile Ala Thr Gly
79 50 55 60
81 Ser Pro Val Ser Thr Glu Leu Gly His Val Leu Ile Glu Ile Ser Ser
82 65 70 75 80
84 Thr His Lys Lys Leu Asn Glu Ser Leu Asp Glu Asn Phe Lys Lys Phe
85 85 90 95
87 His Lys Glu Ile Ile His Glu Leu Glu Lys Lys Ile Glu Leu Asp Val
88 100 105 110
90 Lys Tyr Met Asn Ala Thr Leu Lys Arg Tyr Gln Thr Glu His Lys Asn
91 115 120 125
93 Lys Leu Glu Ser Leu Glu Lys Ser Gln Ala Glu Leu Lys Lys Ile Arg
94 130 135 140
96 Arg Lys Ser Gln Gly Ser Arg Asn Ala Leu Lys Tyr Glu His Lys Glu
97 145 150 155 160
99 Ile Glu Tyr Val Glu Thr Val Thr Ser Arg Gln Ser Glu Ile Gln Lys
100 165 170 175
102 Phe Ile Ala Asp Gly Cys Lys Glu Ala Leu Leu Glu Glu Lys Arg Arg
103 180 185 190
105 Phe Cys Phe Leu Val Asp Lys His Cys Gly Phe Ala Asn His Ile His
106 195 200 205
108 Tyr Tyr His Leu Gln Ser Ala Glu Leu Leu Asn Ser Lys Leu Pro Arg
109 210 215 220
111 Trp Gln Glu Thr Cys Val Asp Ala Ile Lys Val Pro Glu Lys Ile Met
112 225 230 235 240
114 Asn Met Ile Glu Glu Ile Lys Thr Pro Ala Ser Thr Pro Val Ser Gly
115 245 250 255
117 Thr Pro Gln Ala Ser Pro Met Ile Glu Arg Ser Asn Val Val Arg Lys
118 260 265 270
120 Asp Tyr Asp Thr Leu Ser Lys Cys Ser Pro Lys Met Pro Pro Ala Pro
121 275 280 285

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127 305                      310                      315                      320
129 Ser Glu Asp Pro Ser Leu Gln Arg Ser Val Ser Val Ala Thr Gly Leu
130                      325                      330                      335
132 Asn Met Met Lys Lys Gln Lys Val Lys Thr Ile Phe Pro His Thr Ala
133                      340                      345                      350
135 Gly Ser Asn Lys Thr Leu Leu Ser Phe Ala Gln Gly Asp Val Ile Thr
136                      355                      360                      365
138 Leu Leu Ile Pro Glu Glu Lys Asp Gly Trp Leu Tyr Gly Glu His Asp
139                      370                      375                      380
141 Val Ser Lys Ala Arg Gly Trp Phe Pro Ser Ser Tyr Thr Lys Leu Leu
142 385                      390                      395                      400
144 Glu Glu Asn Glu Thr Glu Ala Val Thr Val Pro Thr Pro Ser Pro Thr
145                      405                      410                      415
147 Pro Val Arg Ser Ile Ser Thr Val Asn Leu Ser Glu Asn Ser Ser Val
148                      420                      425                      430
150 Val Ile Pro Pro Pro Asp Tyr Leu Glu Cys Leu Ser Met Gly Ala Ala
151                      435                      440                      445
153 Ala Asp Arg Arg Ala Asp Ser Ala Arg Thr Thr Ser Thr Phe Lys Ala
154                      450                      455                      460
156 Pro Ala Ser Lys Pro Glu Thr Ala Ala Pro Asn Asp Ala Asn Gly Thr
157 465                      470                      475                      480
159 Ala Lys Pro Pro Phe Leu Ser Gly Glu Asn Pro Phe Ala Thr Val Lys
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174 atggtctaga ggctggagat tcaagatctg ggtgccatca ttttctggtt ctgttgatga 180
175 cctcttcca gggtacatac agcttacatc ttgcatcctc aagcgttttt cttataaggc 240
176 taaaaattca caaagcatat atcaatgaat caggaggatc tagatccgga tagtactaca 300
177 gatgtgggag atgttacaaa tactgaagaa gaacttatta gagaatgtga agaaatgtgg 360
178 aaagatatgg aagaatgtca gaataaatta tcacttattg gaactgaaac actcaccgat 420
179 tcaaagtctc agctatcatt gttaattatg caagtaaaat gtttaaccgc tgaactcagt 480
180 caatggcaga aaaaaacacc tgaacaatt cccttgactg aagacgttct cataacatta 540
181 ggaaaagaag agttccaaaa gctgagacaa gatcttgaaa tggtagtctc cactaaggag 600
182 tcaaagaatg aaaagttaaa ggaagactta gaaagggaaac aacgggtggtt ggatgaacag 660
183 caacagataa tggaatctct taatgtacta cacagtgaat tgaaaaataa ggttgaaaca 720
184 ttttctgaat caagaatctt taatgaactg aaaactaaaa tgcttaatat aaaagaatat 780
185 aaggagaaac tcttgagtac cttgggcgag tttctagaag accattttcc tctgcctgat 840
186 agaagtgtta aaaagaaaaa gaaaaacatt caagaatcat ctgtaaacct gataaacctg 900
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190 gttttctttt ttcacacagt aaaaattctt atcattcaag gatattggaa ccacaggact 1140
191 atttggataa aaaacattat ttgcaaatta atgcgcatag tacttttatt gcaaaatggc 1200
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194 tgtaccttac ctcatgcaat attctttgga ttctttgttg atttatgata ttgctaatat 1380
195 aatattttct taaaatatat aacaatatct tttatgcatt tgagttccag ctggtgcttc 1440
196 ttatatatta gaaattataa tgggaaggtc atttaattta cagatgggtt taaaattgag 1500
197 gtaatatctg aggtggcata atttaaaaat atttagcaaa tttgtttcat atatactgtc 1560
198 ttatttctag atttgtttaa aattggaata tgaaaaacta atggataaag ctagcataaa 1620
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200 gattctgcta attattacca acaaaattgt attcatgaca ttttattaat cctctgtgaa 1740
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204 <210> SEQ ID NO: 4

205 <211> LENGTH: 269

206 <212> TYPE: PRT

207 <213> ORGANISM: Homo sapiens

209 <400> SEQUENCE: 4

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214           20           25           30
216 Lys Asp Met Glu Glu Cys Gln Asn Lys Leu Ser Leu Ile Gly Thr Glu
217           35           40           45
219 Thr Leu Thr Asp Ser Asn Ala Gln Leu Ser Leu Leu Ile Met Gln Val
220           50           55           60
222 Lys Cys Leu Thr Ala Glu Leu Ser Gln Trp Gln Lys Lys Thr Pro Glu
223           65           70           75           80
225 Thr Ile Pro Leu Thr Glu Asp Val Leu Ile Thr Leu Gly Lys Glu Glu
226           85           90           95
228 Phe Gln Lys Leu Arg Gln Asp Leu Glu Met Val Leu Ser Thr Lys Glu
229           100          105          110
231 Ser Lys Asn Glu Lys Leu Lys Glu Asp Leu Glu Arg Glu Gln Arg Trp
232           115          120          125
234 Leu Asp Glu Gln Gln Gln Ile Met Glu Ser Leu Asn Val Leu His Ser
235           130          135          140
237 Glu Leu Lys Asn Lys Val Glu Thr Phe Ser Glu Ser Arg Ile Phe Asn
238           145          150          155          160
240 Glu Leu Lys Thr Lys Met Leu Asn Ile Lys Glu Tyr Lys Glu Lys Leu
241           165          170          175
243 Leu Ser Thr Leu Gly Glu Phe Leu Glu Asp His Phe Pro Leu Pro Asp
244           180          185          190
246 Arg Ser Val Lys Lys Lys Lys Lys Asn Ile Gln Glu Ser Ser Val Asn
247           195          200          205
249 Leu Ile Thr Leu His Glu Met Leu Glu Ile Leu Ile Asn Arg Leu Phe
250           210          215          220
252 Asp Val Pro His Asp Pro Tyr Val Lys Ile Ser Asp Ser Phe Trp Pro
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255 Pro Tyr Val Glu Leu Leu Leu Arg Asn Gly Ile Ala Leu Arg His Pro
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264 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
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271 gagcaagttg ggcaagttct ttaaaggggg cggtcttct aagagccgag ccgctcccag 240
272 tccccaggag gccctgggcc gacttcggga gactgaggag atgctgggca agaaacaaga 300
273 gtacctggaa aatcgaatcc agagagaaat cgccctggcc aagaagcacg gcacgcagaa 360
274 taagcgagct gcattacagg cactaaagag aaagaagagg ttcgagaaac agctcactca 420
275 gattgatggc acactttcta ccattgagtt ccagagagaa gccctggaga actcacacac 480
276 caacactgag gtgttgagga acatgggctt tgcagcaaaa gcgatgaaat ctgttcatga 540
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292 taaatatact gtgtctcttt tgggagagcc ttttagtaga ggagtcttat atgagtctct 1500
293 acataagtag tttcacttga gttttgcagt ttgaaatctt aaaggagctt taattgacat 1560
294 ttattatacc aattaagctt ggaatggggc aatggatgca tttcccaaaa cgtgtgaaag 1620
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308 20 25 30
310 Glu Glu Met Leu Gly Lys Lys Gln Glu Tyr Leu Glu Asn Arg Ile Gln
311 35 40 45
313 Arg Glu Ile Ala Leu Ala Lys Lys His Gly Thr Gln Asn Lys Arg Ala

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